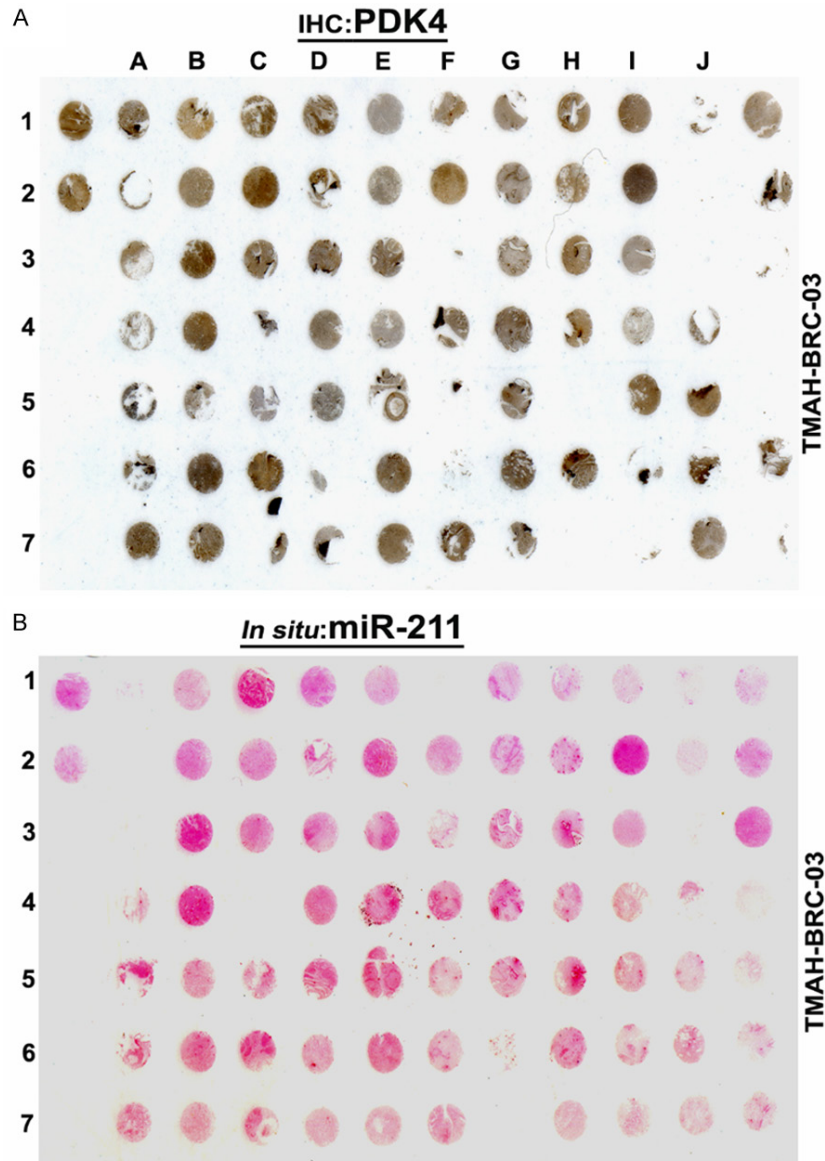


miR-211 and breast cancer

Table S1. List of primers with sequences

PDK4-F	GGAAGCATTGATCCTAACTGTGA
PDK4-R	GGTGAGAAGGAACATACACGATG
HIF1-F	GAAAGCGCAAGTCTTCAAAG
HIF1-R	TGGGTAGGAGATGGAGATGC
GAPDH-F	AATCCCATCACCATCTTCCA
GAPDH-R	TGGACTCCACGACGACTCA
Sox2-F	CAGGAGAACCCCAAGATGCACAA
Sox2-R	AATCCGGGTGCTCCTTCATGTG
TWIST-F	GGACAAGCTGAGCAAGATTCAGA
TWIST-R	TCTGGAGGACCTGGTAGAGGAA
Snail-F	GCTGCAGGACTCTAATCCAGA
Snail-R	ATCTCCGGAGGTGGGATG
hsa-miR-211-F	TTCCCTTTGTCATCCTTCGCCT
Universal Reversal Primer	GTGCAGGGTCCGAGGT



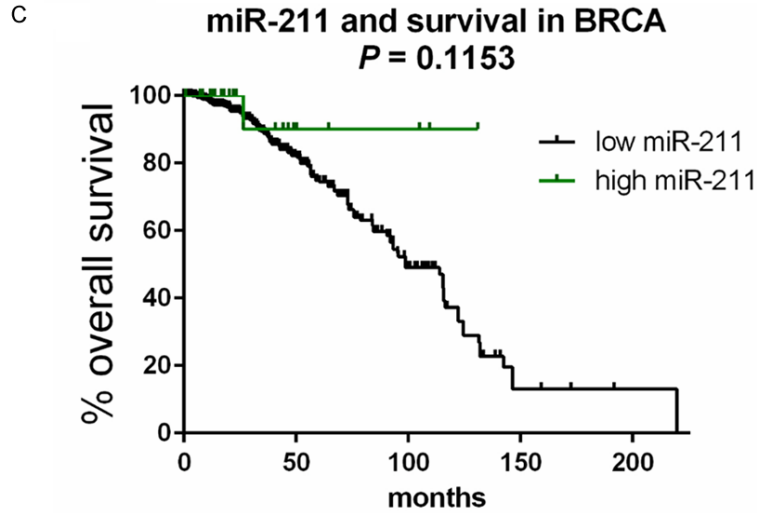


Figure S1. Breast cancer patients show low expression of miR-211. A. Immunohistochemical (IHC) analysis of TMAH-BRC-03 human breast TMA probed for PDK4 expression. B. In situ hybridization assay demonstrating a relative absence of miR-211 RNA in TMAH-BRC-03 TMA. C. Kaplan-Meier survival curve for overall survival of patients with low and high expression of miR-211.

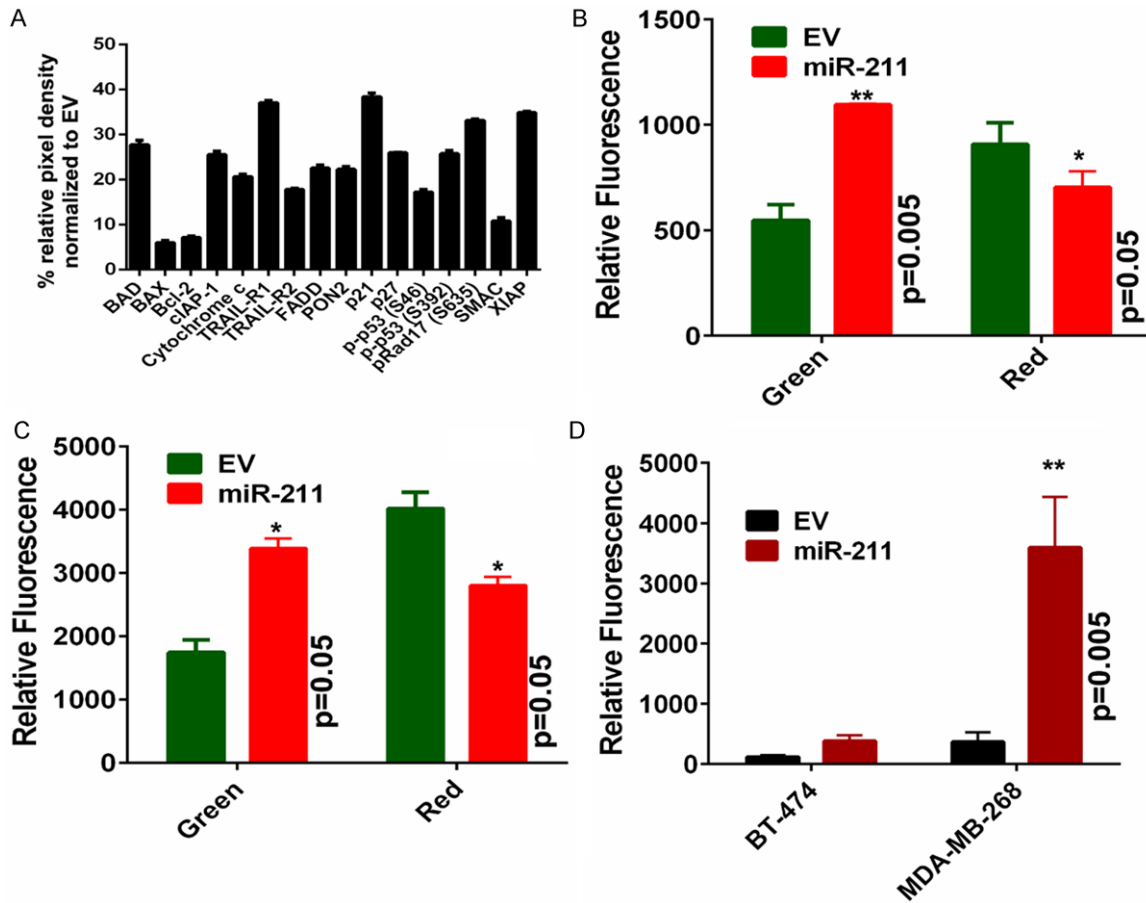


Figure S2. miR-211 overexpression induces apoptosis. A. Quantification of human apoptosis array. The graph is plotted for the apoptotic markers highly expressed in miR-211 treatments compared to the EV. B and C. Quantification of the green fluorescence in the miR-211 treated cells in comparison to red fluorescence of the EV treated cells. Red color suggests the live cells and green color shows the apoptotic cells. D. Quantification of the dead cells using Tunnel assay. The values from control and treated cells were obtained using Image J software.